

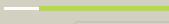
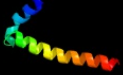
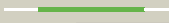




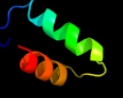











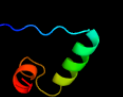


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3098B_(RVBD3098B)_3467409_3467609
 Date Thu Aug 8 16:20:27 BST 2019
 Unique Job ID 1f08553f97abce9d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kxeD_	 Alignment		83.9	30	PDB header: protein binding Chain: D; PDB Molecule: antitoxin protein pard-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
2	c5cegC_	 Alignment		68.4	18	PDB header: toxin Chain: C; PDB Molecule: addiction module antidote protein, cogp/arc/metj family; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
3	d1cuka1	 Alignment		52.3	25	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
4	c1ixrB_	 Alignment		37.9	26	PDB header: hydrolase Chain: B; PDB Molecule: holliday junction dna helicase ruva; PDBTitle: ruva-ruvb complex
5	c2h5xA_	 Alignment		31.0	29	PDB header: dna binding protein Chain: A; PDB Molecule: holliday junction atp-dependent dna helicase ruva; PDBTitle: ruva from mycobacterium tuberculosis
6	c4me7E_	 Alignment		30.9	19	PDB header: hydrolase/hydrolase inhibitor Chain: E; PDB Molecule: antitoxin endoai; PDBTitle: crystal structure of bacillus subtilis toxin mazf in complex with2 cognate antitoxin maze
7	d2b3aa1	 Alignment		27.6	36	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
8	c1xrxD_	 Alignment		25.0	50	PDB header: replication inhibitor Chain: D; PDB Molecule: seqa protein; PDBTitle: crystal structure of a dna-binding protein
9	d1xrxal	 Alignment		25.0	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: SeqA N-terminal domain-like
10	d1v66a_	 Alignment		24.1	28	Fold: LEM/SAP HeH motif Superfamily: SAP domain Family: SAP domain
11	c6qeqD_	 Alignment		20.4	12	PDB header: dna binding protein Chain: D; PDB Molecule: pcf;f; PDBTitle: pcf from enterococcus faecalis pcf10

12	d1ef5a_	Alignment		18.0	38	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
13	c3fmtF_	Alignment		12.6	36	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
14	c6ekrA_	Alignment		12.6	21	PDB header: hydrolase Chain: A: PDB Molecule: type ii site-specific deoxyribonuclease; PDBTitle: crystal structure of type iip restriction endonuclease kpn2i
15	c2z90D_	Alignment		12.3	15	PDB header: dna binding protein Chain: D: PDB Molecule: starvation-inducible dna-binding protein or fine PDBTitle: crystal structure of the second dps from mycobacterium2 smegmatis
16	d1lfda_	Alignment		12.0	36	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
17	c2ba3A_	Alignment		11.7	47	PDB header: dna binding protein Chain: A: PDB Molecule: nika; PDBTitle: nmr structure of nika n-terminal fragment
18	c3kh0A_	Alignment		11.0	36	PDB header: signaling protein Chain: A: PDB Molecule: ral guanine nucleotide dissociation stimulator; PDBTitle: crystal structure of the ras-association (ra) domain of ralgds
19	c4ce4c_	Alignment		10.8	17	PDB header: ribosome Chain: C: PDB Molecule: PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
20	c3w1oA_	Alignment		10.2	58	PDB header: protein binding Chain: A: PDB Molecule: dna mimic protein dmp12; PDBTitle: neisseria dna mimic protein dmp12
21	c4a25A_	Alignment	not modelled	9.8	12	PDB header: metal binding protein Chain: A: PDB Molecule: ferritin dps family protein; PDBTitle: x-ray structure dps from kineococcus radiotolerans in2 complex with mn (ii) ions.
22	d2rgfa_	Alignment	not modelled	8.9	36	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
23	c3l9kZ_	Alignment	not modelled	8.7	40	PDB header: motor protein Chain: Z: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
24	c3l9kX_	Alignment	not modelled	8.7	40	PDB header: motor protein Chain: X: PDB Molecule: dynein intermediate chain, cytosolic; PDBTitle: insights into dynein assembly from a dynein intermediate chain-light2 chain roadblock structure
25	c1qeyD_	Alignment	not modelled	8.3	80	PDB header: gene regulation Chain: D: PDB Molecule: protein (regulatory protein mnt); PDBTitle: nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
26	c1qeyC_	Alignment	not modelled	8.3	80	PDB header: gene regulation Chain: C: PDB Molecule: protein (regulatory protein mnt); PDBTitle: nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
27	c1qeyA_	Alignment	not modelled	8.3	80	PDB header: gene regulation Chain: A: PDB Molecule: protein (regulatory protein mnt); PDBTitle: nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
						PDB header: gene regulation Chain: B: PDB Molecule: protein (regulatory protein mnt);

28	c1qeyB_	Alignment	not modelled	8.3	80	PDBTitle: nmr structure determination of the tetramerization domain2 of the mnt repressor: an asymmetric a-helical assembly in3 slow exchange
29	c2e6oA_	Alignment	not modelled	7.3	27	PDB header: transcription, cell cycle Chain: A: PDB Molecule: hmg box-containing protein 1; PDBTitle: solution structure of the hmg box domain from human hmg-box2 transcription factor 1
30	c3htuE_	Alignment	not modelled	7.0	43	PDB header: protein transport Chain: E: PDB Molecule: vacuolar protein-sorting-associated protein 25; PDBTitle: crystal structure of the human vps25-vps20 subcomplex
31	c2k9iB_	Alignment	not modelled	6.6	27	PDB header: dna binding protein Chain: B: PDB Molecule: uncharacterized protein orf56; PDBTitle: nmr structure of plasmid copy control protein orf56 from sulfobolus2 islandicus
32	c2c6rA_	Alignment	not modelled	6.6	12	PDB header: dna-binding protein Chain: A: PDB Molecule: dna-binding stress response protein, dps family; PDBTitle: fe-soaked crystal structure of the dps92 from deinococcus2 radiodurans
33	d2yw6a1	Alignment	not modelled	6.2	18	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ferritin
34	c2yjkF_	Alignment	not modelled	6.0	15	PDB header: metal-binding protein Chain: F: PDB Molecule: afp; PDBTitle: structure of dps from microbacterium arborescens in the2 high iron form
35	c1hjpA_	Alignment	not modelled	6.0	27	PDB header: dna recombination Chain: A: PDB Molecule: ruva; PDBTitle: holliday junction binding protein ruva from e. coli
36	d1nb9a_	Alignment	not modelled	6.0	38	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
37	c2mdvB_	Alignment	not modelled	5.9	53	PDB header: de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: nmr structure of beta alpha alpha 38
38	c2k5jB_	Alignment	not modelled	5.8	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein yiif; PDBTitle: solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
39	d1mrza1	Alignment	not modelled	5.8	38	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin kinase-like Family: ATP-dependent riboflavin kinase-like
40	d1bvsa1	Alignment	not modelled	5.5	53	Fold: RuvA C-terminal domain-like Superfamily: DNA helicase RuvA subunit, C-terminal domain Family: DNA helicase RuvA subunit, C-terminal domain
41	d1hw1a1	Alignment	not modelled	5.2	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: GntR-like transcriptional regulators